

Figure 1

SEQ ID 8	CTAAGCC	CTCAGAACC	GTCTCGGA	(→)
AF196835	CAACCCAGGAGGACTGGTGAACAAAGCCGCGAAGTGA	TCCATGTAAGCC	CTCAGAACC	GTCTCGGAAGGAGGACCCACATGTTGTAAC
AF260968T.....
AF260969
AF481864
M12294C.....T...G...C.....G..C.T..G.C.....
AF206518
AF317203
AF202541
AF404757T.....
AF404753
AF404754
AF404755
AF404756
AF017254T.....
L48977C.....T...G...C.....G..C.T..G.C.....
AF196536
AF196537T...G..C.....T.....G..C.....
AF196538T...G..C.....T.....GT.C.....
AF196540T...G..C.....T.....GT.C.....
AF196541
AF196542
AF196543T.C.....G...C.....A.....G...T..G.C.....G.....
AF297840T.....C.....A.....G...T..G.C.....G.....
AF458343C.....G.....
AF458344T.....
AF458347T.....
AF458348
AF458350
AF458352T...G..C.....C.....T.....GT.Y.....
AF458353T...G..C.....T.....GT.C.....
AF458355T.....
AF458358T.C.....G...C.....A.....G...T..G.C.....G.....
AF458360
AF458361
AF208017C.....T...G...C.....G..C.T..G.C.....
AF196539C.....T...G...C.....G..C.T..G.C.....
AF196535C.....T...G...C.....G..C.T..G.C.....G.....
AF458359C.....T...G...C.....G..C.T..G.C.....
AF458357C.....T...G...C.....G..C.T..G.C.....
AF458354C.....T...G...C.....G..C.T..G.C.....

AF458349	C.	C.T.	G.	C	G.	C.T.	G.C.
AF458345	C.	T.	G.	C	G.	C.T.	G.C.
AF458346	C.	T.	G.	C	T	G.	C.T.
AF533540	G.	C.T.
AY187012
AY187013
AY187014
AY187015
AY262283
AY277251	AT.T	AT.G.	C.	C	AT	T
AY277252	G
AY278441
AY278442
AY268132
AY268133
AY490240	T
Kunjjin
D00246	T	A	G
AY274504	T	A	G
AY274505	T	A	G
L49311	T	A	G
L48978	T	A	G
L48979	T	A	G
AF297840	T	A	G
AF297841	T	A	G
AF297842	T	A	G
AF297843	T	A	G
AF297844	T	A	G
AF297845	T	A	G
AF297846	T	A	G
AF297847	T	A	G
AF297848	T	A	G
AF297849	T	A	G
AF297850	T	A	G
AF297851	T	A	G
AF297852	T	A	G
AF297853	T	A	G
AF297854	T	A	G
AF297855	T	A	G
AF297856	T	A	G
AF297857	T	A	G
AF297858	T	A	G
AF297859	T	A	G

AF458351T.....G.A.....G.....G.....
AF458356T.....C.....A.....G.....
L24512T.....A.....G.....
JEV		
AB051292	GTT.....T.....	T.T.AC.CG.AGGTGG.A.....C.T..TG.GCACC.G.G.G.....
AF014160	GT.....T.....	T.T.AC.TA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF014161	GT.....T.....	T.T.AC.TA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF045551	GTT.....T.....	T.T.AC.CG.AGGTGG.A.....C.T..TG.TCAC.G.G.G.....
AF069076	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF075723	GT.....C.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF080251	GT.....T.....	T.T.AC.CA.AAGTGA.A.....G.....TG.TCAC.G.G.G.....
AF098735	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF098736	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF098737	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF217620	GTT.....T.....	T.T.AC.CA.AGGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF221499	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF221500	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF254452	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF254453	GT.....A.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
AF315119	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF416457	GT.....T.....	T.T.AC.CAA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF486638	GT.....T.....	T.T.AC.CA.AAGTGA.A.....C.T..TG.TCAC.G.G.G.....
U14163	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
U15763	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
L48961	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
U47032	GT.....T.....	T.T.AC.CG.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
M18370	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
M55506	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
D90195	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
D90194	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF311748	GT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.G.....
AF092550	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF092552	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF092553	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF139531	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF148900	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF148901	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF148902	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF218068	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
AF289816	GT.....T.....	T.T.AC.CG.AGGTGG.A.....T.T..TG.TCAC.G.G.G.....
AF318291	GT.....T.....	T.T.AC.CG.AGGTGG.A.....T.T..TG.TCAC.G.G.G.....
L48967	GTT.....T.....	T.T.AC.CA.AAGTGA.A.....T.T..TG.TCAC.G.G.GG.....
L48968	GTT.....T.....	T.T.AC.CA.AAGTGA.A.C.....T.T..TG.TCAC.G.G.GG.....

AY184212	GT	C	T.T.AC..CG..GAGTGA.A		A..T..TG.TCAC..G.TG..GG...
AY251616	GT	T	T.T.AC..CG..AGGTGG.A		T..T..TG.TCAC..G..G....
AY278556	GTT	T	T.T.AC..CG..AGGTGG.A		C..T..TG.TCAC..G..G....
AY316157	GTT	T	T.T.AC..CG..AGGTGG.A		C..T..TG.TCAC..G..G....
L54067	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54068	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54069	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54070	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54071	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54072	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54122	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
L54123	GTT	T	T.T.AC..CA..AGGTGA.A		T..T..TG.TCAC..G..G....
AF306514	GTT	T	TTT.AC..CG..AGGTGG.A		CTCCT...TT.TCAC..G..G....
AF306515	GT	C	TTT.AC..CA..AAGTGA.A		T..T..TT.TCAC..G..G....
AF306516	TT	T	TTT.AC..CA..AAGTGA.A		T..T..TT.TCAC..G..G....
AF306517	GT	T	T.T.AC..CA..AGGTGA.A		T..T..TT.TCAC..G..G....
SLEV					
BFS1750-C	TGG	T	AATCT.GCCGAGT GCA	TT..A..G..GTCC.TAGCACGTAG.CTGGAGAGG.C	
1750-Std	TGG	T	AATCT.GCCGAGT GCA	TT..A..G..GTCC.TAGCACGTAG.CTGGAGAGG.C	
TD6-4G-C	TGG	T	AATCT.GCCGAGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
TD6-4G-20	TGG	T	AATCT.GCCGAGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
CoaV750	TGG	T	AATCT.GCTGAGT GCA	TT..AT..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
L695121.05	TGG	T	AATCC.GCTGGGT GCA	TT..A..G..GTCC.TGGCATGTAG.CTGGAGAGG.C	
TNM771K-C	TGG	C	AATCT.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
MSI-7-C	TGG	T	AATCC.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
Kern217	TGG	T	AATCC.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
CoaV608	TGG	T	AATCC.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
TBH-28	TGG	T	AATCC.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAGAGG.C	
VR1265	TGG	T	AATCT.GCTGGGT GCA	TT..A..G..GTCC.TGGCACGTAG.CCGGAGAGG.C	
CoaV353		T	AATCTAGCTGAGT GCA	TT..A..G..GTCC.TGGCACGTAG.CTGGAG.GG.C	
MVEV					
VR77					
AF161266		T	ATTCTCC.CGGTTG.A	AG.AGT...TGCCAACAATGGAGATG.A	
M35172		T	ATTCTCC.CGGTTG.A	AG.AGT...TGCCAACAATGGAGATG.A	
L48972		T	ATTCTCC.CGGTTG.A	AG.AGT...TGCCAACAATGGAGATG.A	
L48973		T	ATTCTCC.CGGTTG.A	AG.AGT...T.CCAACAATGGAGATG.A	
L48974		T	ATTCTCC.CGGTTG.A	AG.AGT...TGCCAACAATGGAGATG.A	
L48975		T	ACTCTCT.CGGTTG.A	AG.AGT...TGCCAACAATGGAGATG.A	
L48976		T	ACTCTCT.CGGTTG.A	AG.AGT...TTCCAACAATGGAGATG.A	
Koutango virus		T	ATTCTCC.CGGTTG.A	AG.AGT...TGC.AACAATGGAGATG.A	
L48980		C	T.T...G.A...C...T..G....T..TTC.....	

SEQ ID 74

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AF416457	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
AF486638	CCC.C	AGG.T	A.	CAT	TTG.T	A.T.G.
U14163	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
U15763	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
L48961	CTC.C	AGG.T	A.	CAT	TTG.T	A..G.
U47032	CCC.C	AGG.T.G	A.	CAT	TTG.T	A..G.
M18370	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
M55506	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
L78128	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
D90195	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
D90194	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
AF311748	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
AY184212	CCCT.C	AAG.T	A.	CAT	TTG.T	A..G.
AY316157	CCC.C	AGG.T	A.	CAA	TTG.T	A..G.
AF306514	CCC.C	AGG.T.T	A.	CAA	TTG.T	A..G.
AF306515	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
AF306516	CCC.C	AGGG.T	A.	CAT	TTG.T	A..G.
AF306517	CCC.C	AGG.T	A.	CAT	TTG.T	A..G.
D00037	CCT.T.T	T.T.AGGT.TT	T.T	CT	TTG.T	A..G.
M14933	CCT.T.T	T.T.AGGT.TT	T.T	CT	TTG.T	A..G.
SLEV						
BFS1750-C	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
1750-Std	CCG.C	AGAC.G	A.	C.GA		
TD6-4G-C	CCG.C	AGAT.G	A.	T..G.TT..G.	A.	A.
TD6-4G-20	CCG.C	AGAT.G	A.	T..G.TT..G.	A.	A.
CoaV750	CCG.C	AGAT.G	A.	C.G		
L695121.05	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
TNM771K-C	CCG.C	AGAC.G	A.	T..G.TT..G.	A.N.	A.
MSI-7-C	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
Kern217	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
CoaV608	CCG.CA	AGAC.G	A.	T..G.TT..G.	A.	A.
TBH-28	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
VR1265	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
CoaV353	CCG.C	AGAC.G	A.	T..G.TT..G.	A.	A.
MVEV						
VR77	CG.C	A.G.G.T.C	A.	ACT.T	C..G.AT..	AA.
AF161266	CG.C	A.G.G.T.C	A.	ACT.T	C..G.AT..	AA.
M35172	CG.C	A.G.G.T.C	A.	ACT.T	C..G.AT..	AA.

Figure 3*

SEQ ID 70	CCCCCTTCCTGATCTCCAATCTCCTCTGGG					CCCCCTTCCTGATCTCCAATCTCCTCTGGG
(←)						
ID 28	GGACTAGAGGTTAGAGGAGACCCGCGG					GGACTAGAGGTTAGAGGAGACCCGCGG
AF196835	CAGCGGAPAGGAGTAGGCTTAGAGGAGGCGCGG					
GGAGGAGTAGAGGCTTAGGAGGCGCGCTGCCACAAACA						
West Nile virus						
AF260967	TT	TAAAGT	GC	A	CGGCCAGCCTGACT GAAGCTGTAGGTCAAG
.....G..
AF260968
.....
AF260969	G....G..
.....
AF481864
.....
M12294A...G.....T	AAAA.T..G..
.....A.....A..CACA.C..A.
AF206518G..
.....
AF317203	G....G..
.....
AF202541G..
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AF404757	G...AG..
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AF404753G..
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AF404754G..
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AF404755G..
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AF404756G..
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AF017254
.....
AF208017A..G.....T.....A..T	.AAA.T..G..
AF533540G..
.....
AY262283G.....	...	G....G..
.....
AY277251A..A..G.....C.....T...CATA..AG	AGAG..AGAG..A.....
AY277252	G....
AY278441	G....G..
.....
AY278442	G....
AY268132	G....G..
.....

AY268133G..
 AY490240
 Kunjin virus
 AY274504 ...A.T.....T.C.G....
G.....
 AY274505 ...A.T.....T.C.G....
G.....
 L24512 ...A.T.....T.C.G....
G.....
 Japanese encephalitis virus
 AB051292 .TA..T.T.....T.. AAA C.CA TT .TG.....AG.CCC..
 C.....G.AGG..T.....A.....CAATTGC.TCA.
 AF014160 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF014161 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF045551 TTA..T.T.....T.. AAA C.AA TT .TG.....AG.CCC..
 C.....AGG..T.T.. A.....CAATTGC.T..
 AF069076 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF075723 .GA..T.T.....T.. AAA T.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF080251 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF098735 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CTC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF098736 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF098737 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF217620 .GA..T.T.....T.. AAA C.CA AT .TG.....AG..TC..
 C.....AGG.A.T.....A.....CAATTGC.TCA.
 AF221499 .GA..T.T.....T.. AAA C.TA A. .TG.....AG.CTC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF221500 .GA..T.T.....T.. AAA C.TA A. .TG.....AG.CTC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF254452 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF254453 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF315119 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF416457 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 AF486638 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.
 U14163 .GA..T.T.....T.. AAA C.CA A. .TG.....AG.CCC..
 C.....AGG..T.....A.....CAATTGC.TCA.

U15763	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
L48961	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CTC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
U47032	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T..G.....	A.....	CATTGC.TCA.				
M18370	.GA..T.T.....T..	AAA	C..CA	AT		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
M55506	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
L78128	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
D90195	.GA..T.T.....T..	AAA	C..CA	AT		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
D90194	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF311748	.GA..T.T.....T..	AAA	C..CA	A.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AY184212	.GA..AT.T.....T..	AAA	C..CA	A.		.TG.....AG.CCCT.
C.....	AAG..T.....	A.....	CAT.TGC.TCA.				
AY316157	.TA..T.T.....T..	AAA	C..CA	T.		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CAATTGC.T..				
AF306514	TTA..T.T.....T..	AAA	C..AA	TT		.TG.....AG.CCC..
C.....	AGG..T.T..A.....	A.....	CAATTGC.T..				
AF306515	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF306516	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
AF306517	.GA..T.T.....T..	AAA	C..AA	AA		.TG.....AG.CCC..
C.....	AGG..T.....	A.....	CATTGC.TCA.				
St. Louis encephalitis virus							
BFS1750	..T...T.....T..	CA	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
1750-Std	..T...T.....T..	CA	.CTTG	..		.A.....AA.CCG..C
TD6-4G	..T...T.....T..	CA	.CTCG	..		.A.....AA.CCG..C
.....	AGAT..G.....	A.....	T...GTT..CGC				
Coav750	..T...T.....T..	CA	.CTTG	..		.A...A.AA.CCG..C
L695121.05	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
TNN771K	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				
MSI-7	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
Kern217	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
Coav608	..T...T.....T..	.A	.CTTG	..		.A.....AA.CCG..C
A.....	AGAC..G.....	A.....	T...GTT..CGC				
TBH-28	..T...T.....T..	.A	.TTTG	..		.A.....AA.CCG..C
.....	AGAC..G.....	A.....	T...GTT..CGC				

VR1265 ..T...T.....T.....T..A..CTTG .. . A.....AA.CCG..C
AGAC..G.....A.....T....GTC..CGC
 CoaV353 ..T...T.....T.....T..CA..CTTG .. . A.....AA.CCG..C
AGAC..G.....A.....T....GTT..CGC
 Murray Valley encephalitis virus
 VR77 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 AF161266 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 M35172 ..CC.....T.....T....AAGA G T.....AG..CG.CA.G.G..T..C.....A.....ACT.T
GC
 Dengue virus type 1
 U88537 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.GG
 U88536 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.GG
 U88535 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.GG
 M87512 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....TCCTG.TG.T.....A.....CG..ATA.C..T. GCGG.....A.ACC.GG
 AY206457 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A
 AY145123 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A
A.....CC..ACA.C....
 AY145122 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....AG.CAGGA
 G.....CTC.T.T.....A.....CC..ACA.C.... GCGG.....AG.CAGGA
 AY145121 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....AG.CAGGA
 G.....CTC.T.T.....A.....CC..ACA.C.... GCGG.....A.ACC.GG
 AF514889 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.TG
 AF514885 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ATA.C.... GCGG.....A.ACC.TG
 AF514883 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ATA.C.... GCGG.....A.ACC.GG
 AF514878 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.TG
 AF514876 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ATA.C.... GCGG.....A.ACC.GG
 AF513110 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.TG
 AF350498 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T. GCGG.....A.ACC.TG
 AF311958 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..TCA.C.... GCGG.....A.ACC.TG
 AF311957 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.TG
 AF311956 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ACA.C.... GCGG.....A.ACC.GG
 AF310148 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG G.....CCTG.TG.T.....

AF310147 AT...GT.GCA.....T.....T.CCAAAAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T.
 AF310146 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ACA.C....
 AF309641 AT...GT.GCA.....T.....T.CGAAAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T.
 AF298808 AT...GT.GCA.....T.....T.CCAAAAC AC..CGCAGCA GCGG.....A.ACC.GG
 G..T.....CCTG.TG.T.....A.....CC..ATA.C..T.
 AF298807 AT...GT.GCA.....T.....T.CCAAAAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ACA.C....
 AF226687 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C....
 AF226686 AT...GT.GCA.....T.....T.CCAAGAC AT..CGCAGCA GCGG.....A.ACC.GG
 G.....CC.TG.TG.T.....A.....CC..ACA.C....
 AF226685 AT...GT.GCA.....T.....T.CCTAGAC AT..CGCAGCA GCGG.....A.ACC.TG
 G.....CC.TG.TG.T.....A.....CC..ACA.C....
 AF180818 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..GTA.C..T.
 AF180817 AT...GT.GCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..GTA.C..T.
 AB074761 AT...GTGCA.....T.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 GA.....CCTG.TG.T.....A.....CC..ATA.T..T.
 AB074760 AT...GT.GCA.....T.....T.CCAAAAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T.
 VR344-3 AT...GT.GCA.....AT.....T.CCAAGAC AC..CGCAGCA GCGG.....A.ACC.GG
 G.....CCTG.TG.T.....A.....CC..ATA.C..T.
 Dengue virus type 2
 AF022434 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C.GA.
 AF022435 AT...CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022436 AT...CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022437 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022438 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022439 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022440 AT...CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF022441 AT...CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF038402 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF038403 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF100145 AT...CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.T..A.

AF100146 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 AGC..A.
 AF100147 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100148 AT..TGT.GT.....C.....T.CCTT C AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF100149 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....CCTCACT.....A.....CCCAA
 A.C..A.
 AF100150 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF100151 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 G.C..A.
 AF100458 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100459 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100460 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100461 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100462 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100463 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100464 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AGGCA.GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF100465 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 G.C..A.
 AF100466 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
 A.T..A.
 AF100467 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100468 AT..CGT.GT.....C.....T.CCTT AC AG.TCGAGCAACAATGGG.....AGG...GA
 T.....TCTCACT.....A.....CCCAA.A.C..A.
 AF100469 AT..CGT.GT.....C.....T.CCTT C AG.TCGAGCAACAATGGG.....TGG...GA T.....TCTCACT.....A.....CCCAA
 A.C..A.
 AF119661 AT..CGT.GG.....C.....T.CCTT AC A..TCGAGCAACAACGGG.....AGG...GA T.....TCTCACT.....ATT.....CCCAA
 A.C..A.
 AF169687 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169678 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169688 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
 A.C..A.
 AF169679 AT..CGT.GT.....C.....T.CCTT AC A..TCGAGCAACAATGGG.....AAG...GA T.....TCTCACT.....A.....CCCGA
 A.C..A.
 AF169680 AT..CGT.GT.....C.....T.CCTC AC A..TCGAGCAACAATGGG.....AGGC..GA T.....TCTC.CTT.....A.....CCCGA
 A.C..A.

AF169681 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169682 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169683 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169684 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169685 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF169686 AT..CGT.GT.....C.....T.CCTC AC A..TCGCAGCAACAATGGG.....AGGC..GA T.....TCTC.CT.....A.....CCCGA
A.C..A.
AF204177 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF204178 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF208496 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.
AF276619 AT..CGT.GT.....C.....T.CCTT GC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309950 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309951 AT..CGT.GT.....C.....T.CCTT AC AG.TCGCAGCAACAACGGG.....AGG...GA TA.....TCTCACC.....A.....CCCAA
A.C..A.
AF305592 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309953 GT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAAAAATGGG.....AGG..TG.
T.....CCCACT.....A.....CCAG.....A.
AF309954 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAAAAATGGG.....AGG..TG.
T.....CCCACT.....A.....CCAG.....A.
AF309955 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309956 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309957 AT..TGT.GT.....C.....T.CCTT AA G..TCGCAGCAA AATGGG.....AGG..TG.
T.....CCCACT.....C.....A.....CCAG.....A.
AF309958 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309959 AT..TGT.GT.....C.....T.CCTT AA A..TCGCAGCAAAAATGGG.....AGG..TGG T.....CCACATT.....A.....CCCAG
AC...A.
AF309960 AT..CGT.GT.....C.....T.CCTT AC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309961 AT..TGT.GT.....C.....T.CCTT AA GG.TCGCAGCAA AATGGG.....AGG..TGG T.....CCCACT.....A.....CCCA.
A..T.AT
AF309962 AT..CGT.GT.....C.....T.CCTT GC A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.
AF309963 AT..CGT.GT.....C.....T.CCTT AC A..GTGCAGCAGCAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.

AF309964	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.		
AF309965	AT..CGT.GT.....C.....T.CCTT C	AG.TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
AF359579	AT..CGT.GT.....C.....T.CCTT GC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCGA
A.T..A.		
AF489932	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
AJ487271	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
AY037116	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.A.....A.....CCCGA
A.T..A.		
M19197	AT..CGT.GT.....C.....T.CCTT AC	AG.TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M20558	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAACGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M29095	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGG...GA T.....TCTCACT.....A.....CCCAA
A.C..A.		
M84727	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
M84728	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61245	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C.GA.		
U61246	AT..CGT.GT.....C.....T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61247	AT..CGT.GT.....C.....T.CCTC AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U61248	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U87411	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
U87412	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TCTC.CT.....A.....CCCGA
A.C..A.		
VR345-2	AT..CGT.GT.....C.....T.CCTT AC	A..TCGCAGCAACAATGGG.....AGGC.GA T.....TC.C.CT.....A.....CCCGA
A.C..A.		
<u>Dengue virus type 3</u>		
AF310149	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
M93130	AC..TGT.GCA.....T.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....TA.....CC..A
A.C... .		
AF317645	AC..TGT.GCA.....T.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....TA.....CC..A
A.C... .		
AY099336	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
AY099337	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		
AY099343	AC..TGT.GCA.....C.....T.CCATGAC	AC..CGCAGCA GCGG.....GAG.ACTGAGG.....CC..CTTGCA.....A.....CC..A
A.T... .		

AY099344	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T..							
AY099345	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T..							
AY099346	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T..							
AY099347	AC..TGT.GCA.....C.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	A.....	CC..A
A.T..							
VR1256-3	AC..TGT.GCA.....T.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	TA.....	CC..A
A.C..							
VR1256-5	AC..TGT.GCA.....T.....	T.CCATGAC	AC..CGCAGCA	GCGG.....GAG.ACTGAGG.....	CC..CTTGCA.....	TA.....	CC..A
A.C..							
Dengue virus type 4							
M14931	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AF289029	GT..CAT.TT.....C.....	T.CCATCACCACA...	CGCAGCAAAAA	GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AF310150	GT..CAT.TT.....T.....	T.CCATTA.CAACA...	CGCAGCAC	AA.GGG.....GAAG.C.GGAT.....	CTC.T.AT.....		
AF310152	GT..CAT.TT.....T.....	T.CCATTA.CAACA...	CGCAGCAC	AA.GGG.....GAAG.C.GGAT.....	CTC.T.AT.....		
AF310153	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AF326573	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AF326825	GT..CAT.TT.....C.....	T.CCATCACTGATA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AF326826	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....A		A.....	CCCAACA
C..							
AF326827	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....A		A.....	CCCAACA
C..							
AF375822	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152039	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152043	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152047	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152051	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152055	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152059	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152063	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152067	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							
AY152071	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T.T.....	A.....	CCCAACA
C..							

[illegible]

[illegible]

[illegible]

AY152171	GT..CAT.TT.....C.....	T.CCATCACTGACA...	CGCAGCA	AA.GGG.....GAAGCC.GGAG.....	CTC.T..T.....	A.....	CCCAACA
C...:							
VR217-1	GT..CAT.TT.....C.....	T.CCATCACTAACA...	CGCAGCA	AAAGGGG.....GAAGCC.GGAG.....	CTC.T..T.....	A.....	CCCAACA
C...:							

*Two potential binding sites for SEQ ID NOS.: 28 & 70 can be found in this region. These are denoted by single underline for SEQ ID NO.: 28, and shading for SEQ ID NO.: 70.

KY1129 5'-GTAAGCC CTCAGAACCGTCTCGGAA-3'

WNV

AF317203
AF196835
AF260967
AF260968
AF260969
AF481864
M12294
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254
L48977
AF196536
AF196537
AF196538
AF196540
AF196541
AF196542
AF196543
AF458343C.....
AF458344
AF458347
AF458348
AF458350
AF458352C.....
AF458353
AF458355
AF458358
AF458360
AF458361
AF208017
AF196539
AF196535
AF458359
AF458357
AF458354
AF458349
AF458345
AF458346T.....T.....
AF533540

JEV

AB051292	.A.....
AF014160	.A.....
AF014161	.A.....
AF045551	.A.....
AF069076	.A.....
AF075723	.A.....
AF080251	.A.....G.....
AF098735	.A.....
AF098736	.A.....
AF098737	.A.....
AF217620	.A.....
AF221499	.A.....
AF221500	.A.....
AF254452	.A.....
AF254453	.A.....
AF315119	.A.....T.....
AF416457	.A.....
AF486638	.A.....
U14163	.A.....
U15763	.A.....

Fig. 4A

KY1129 5'-GTAAGCC CTCAGAACCGTCTCGGAA-3'

JEV cont.

L48961	.A.....
U47032	.A.....
M18370	.A.....
M55506	.A.....
L78128	.A.....
D90195	.A.....
D90194	.A.....
AF311748	.A.....
AF092550	.A.....
AF092552	.A.....
AF092553	.A.....
AF139531	.A.....
AF148900	.A.....
AF148902	.A.....
AF218068	.A.....
AF289816	.A.....
AF318291	.A.....
L48967	.A.....
L48968	.A..C.....
L54067	.A.....
L54068	.A.....
L54069	.A.....
L54070	.A.....
L54071	.A.....
L54072	.A.....
L54122	.A.....
L54123	.A.....
AF306514	.A.....
AF306515	.A.....T.....
AF306516	.A.....T.....
AF306517	.A.....A.....T.....

MVEV

AF161266	.A.....T.C.....
M35172	.A.....T.C.....
L48972	.A.....T.C.....
L48973	.A.....T.C.....
L48974	.A.....T.C....C.....
L48975	.A.....T.C.....
L48976	.A.....T.C.....T.....

KUNJIN

AF458351G.
AF458356
AF297840C.....
AF297841
AF297842
AF297843
AF297844
AF297845
AF297846C.....
AF297847C.....
AF297848
AF297849
AF297850C.....
AF297851C....GT
AF297852C.....
AF297853C.....
AF297854
AF297855
AF297856
AF297857G.....
AF297858
AF297859
L48978
L49311
D00246
L48979
L24512

KOUTANGO

L48980
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Fig. 4B

KY1130 5'-TCCTAGTCTA TCCCAGGTGTCAA-3'

WNV

AF196835
AF260967
AF260968
AF260969
AF481864
M12294	C.....
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254A.....
L24512

JEV

AB051292	...C.....T.....
AF014160	...C.....T.....
AF014161	...C.....T.....
AF045551	...C.C...T.....
AF069076	...C.....T.....
AF075723	...C.....T.....
AF080251	...C.....T.....
AF098735	...C.....T.....
AF098736	...C.....T.....
AF098737	...G.....TCT.....
AF217620	...C.....T.....
AF221499	...C.....T.....
AF221500	...C.....T.....
AF254452	...C.....T.....
AF254453	...C.....T.....
AF315119	...C.....T.....
AF416457	...C.....T.....
AF486638	...C...A..T.....
U14163	...C.....T.....
U15763	...C.....T.....
L48961	...C.....T.....
U47032T.....
M18370	...C.....T.....
M55506	...C.....T.....
L78128	...C.....T.....
D90195	...C.....T.....
D90194	...C.....T.....
AF311748	...C.....T.....
AF306514	...C.C...T.....
AF306515	...C.....T.....
AF306516	...C.....T.....
AF306517	...C.C...T.....
D00037	...C.....T.....
M14933	...C.....T.....

MVEV

AF161266TT.....
M35172TT.....

Fig. 4C

KY1131 5' -GGACTAGAGGTTAGAGGAGACCCCGCGG-3'

WNV

AF196835
AF260967
AF260968
AF260969
AF481864
M12294T
AF206518
AF317203
AF202541
AF404757
AF404753
AF404754
AF404755
AF404756
AF017254
AF208017T.....A..T
L24512T

JEV

AB051292T..
AF014160T..
AF014161T..
AF045551T..
AF069076T..
AF075723T..
AF080251T..
AF098735T..
AF098736T..
AF098737T..
AF217620T..
AF221499T..
AF221500T..
AF254452T..
AF254453T..
AF315119T..
AF416457T..
AF486638T..
U14163T..
U15763T..
L48961T..
L24512
U47032T..
M18370T..
M55506T..
L78128T..
D90195T..
D90194T..
AF311748T..
AF306514T..
AF306515T..
AF306516T..
AF306517T..

MVEV

AF161266A.TC
M35172A.TC

Fig. 4D

KY1131 5' -GGACTAGAGGTTAGAGGAGACCCCGCGG-3'

DENGUE

AF226685C..C
AF311956C..C
AF311957C..C
AF311958C..C
AY145121C..C
AY145122C..C
AF514878C..C
AF514885C..C
AF514889C..C
AF489932C.CA
AF226687C..C
AX224213C.C.
AX224215C.C.
AX224217C.C.
AX224219C.C.
AX224225C.C.
AX224227C..C
AX224233C..C
AB074760C..C
AB074761C..C
A75711CG.C
AX224221C.C.
AX224223C.C.
U87412C.C.
U61246C.C.
U61247C.C.
AF100465C.CA
AF100466C.CA
AX224209C..C
AF180818C..C
AF326573C.CA
AF350498C..C
AF359579C.C.
AY037116C.C.
AF309950C.C.
AF309953C.CA
AF309954C.CA
AF309959C.CA
AF309962C.C.
AF309963C.C.
AF309964C.C.
AF309965C.CA
AF289029C.CA
AF208496C.CA
AF310146C..C
AF310149C..C
AF310153C.CA
AF226686C..C
AF276619C.C.
AF169678C.C.
AF169679C.C.
AF169680C.C.
AF169681C.C.
AF169682C.C.
AF169683C.C.
AF169684C.C.
AF169685C.C.
AF169686C.C.
AF169687C.C.
AF169688C.C.
AF100145C.CA
AF100467T.CC
AF100468T.CC
AF100149T.CC
M20558C.CA
M29095C.CA
M19197C.CA
M14931C.CA
U87411C.C.
U88536C..C

Fig. 5A

KY1131 5'-GGACTAGAGGTTAGAGGAGACCCCGCGG-3'

DENGUE, cont.

U88537C..C
AF038403C.CA
AF326826C.CA
AF326827C.CA

MONTANA MYOTIS LEUKOENCEPHALITIS VIRUS

NC_004119TTCC
-----------	-----------

MODOC VIRUS

NC_003635CG.C
-----------	-----------

YELLOW FEVER VIRUS

X03700	..T.....TC.A.
U52393	..T.....TC.A.
U52407	..T.....TC.A.
AF052448	..T.....TC.A.

Fig. 5B

FIGURE 6

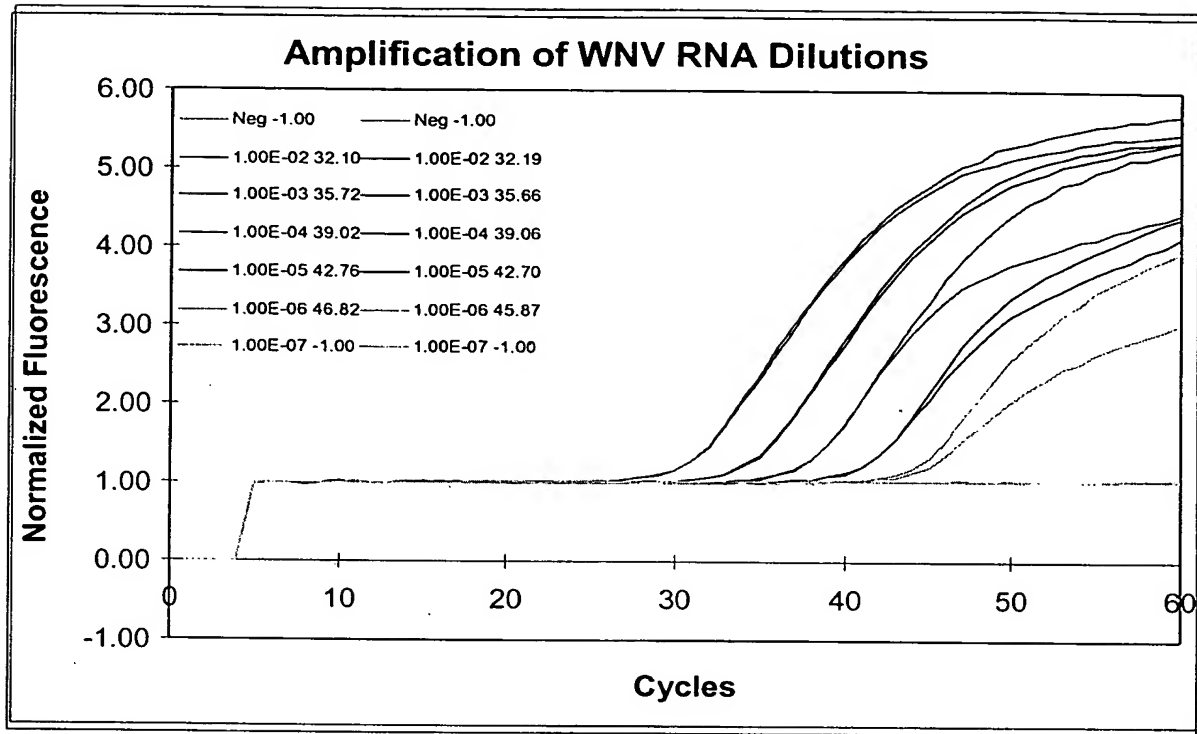


Figure 7

BFS1750	TTGCCACCGGATGTCAGGTAAACGGTGCTGTCTGTAAACCTGGCCCCCAGGTGACTGGGTTATCAAAGCCAATCTGGCCGAGTGCAAAGCCC	90
1750-Std	
TD6-4GC.....	
CoaV750C.....C.....T.....	
L695121.05	C..T.G.....
TNM771KC.....	T.G.....
MSI-7C.....C.....C..T.G.....	
Kern217C.....C.C..T.G.....	
CoaV608C.....C.C..T.G.....	
TBH-28C.C..T.G.....	
VR1265A.....T.G.....	
CoaV353A..T.....	
BFS1750	CTCATTCGGACTCGGGAGGTCCTTAGCACGTAGCTGGAGAGGACGCAAAAGTCAGACCAGAAATGCCACCTGAAAGCATGCTAAAGGT	180
1750-StdG.....	
TD6-4GG.....	
CoaV750	...G...T.....G.....	
L695121.05G..T....C.....	
TNM771KG...C.....	
MSI-7G...C.....	
Kern217G...C.....	
CoaV608G...C.....	
TBH-28G.....C.....C.....	
VR1265G.....C.....C.....	
CoaV353G.....	
BFS1750	GCTGTCTGTACATGCCCCAGGAGGACTGGGTTAAACAAAGCTTAACAGCCCCCAGGGCCCCAACCATGGAGTGCGTGACCATGGCGTAAGG	270
1750-Std	
TD6-4G	
CoaV750	
L695121.05	
TNM771KA.....	
MSI-7	
Kern217	
CoaV608	

TBH-28
VR1265
CoaV353

BFS1750 ACTAGAGGTTAGAGGAGACCCCGCTGCAACTTGGCAAGGCCCAACCCGCTCGAAGCTGTAGAGACGGGGGAAGGACTAGAGGTTAGAGG 360
1750-Std
TD6-4G
CoaV750
L695121.05
TNM771K
MSI-7
Kern217
CoaV608
TBH-28
VR1265
CoaV353

BFS1750 AGACCCCTTGCCGTTAACGCAAAACAACAGCATATTGACACCTTGAAAGACAGGAGATC 418
1750-Std
TD6-4G
CoaV750
L695121.05
TNM771K
MSI-7
Kern217
CoaV608
TBH-28
VR1265
CoaV353